ABSTRACT  Plasminogen Activator Inhibitor-1 (PAI-1) gene is located at 7q.21.3-22 and its polymorphism is functionally important in regulating the gene expression. A single basepair insertion (GGGGG) / deletion (GGGG) polymorphism at 675 base pair of the promoter region PAI-1 gene has been reported. Homozygous individual for the 4G allele have higher basal and inducible concentrations of PAI-1 plasma than those with one or two copies of the 5G allele. High PAI-1 levels have been associated with adverse outcome of DSS patients. The aim of this study was to identify PAI-1 gene polymorphism in Dengue Hemorrhagic Fever (DHF) patients and healthy participants with special reference to the possible correlation between severity of the disease and its polymorphism. A descriptive observational method was used involving forty subjects consisted of twenty each DHF patients and healthy participants. Blood samples were collected from patients admitted at Dr. Kariadi Hospital and healthy participants from Balita Sehat at the Puskesmas Pandanaran. Restriction Fragment Length Polymorphism was employed following Polymerase Chain Reaction to identify the PAI-1 gene polymorphism. It was shown that in DHF patient, four subjects (20%) were 4G/4G homozygote, four subjects (20%) were 4G/5G heterozygote and twelve subjects (60%) were 5G/5G homozygote. In healthy participants four subjects (20%) were 4G/4G homozygote, ten subjects (50%) were 4G/5G heterozygote, and six subjects (30%) were 5G/5G homozygote. Chi-square test showed that polymorphism in DHF patients did not significantly differ with healthy participants [p>0.05]. Further study with bigger sample size and taking into consideration the degrees of severity of the disease should be done.